RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/445,223A_

Source: _/FW/6_

Date Processed by STIC: _5/6/05_

ENTERED

RAW SEQUENCE LISTING   DATE: 05/06/2005
PATENT APPLICATION: US/09/445,223A   TIME: 15:22:14

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\05062005\I445223A.raw

```
 3 <110> APPLICANT: WALLACH, David
 4        BOLDIN, Mark
 5        MALININ, Nikolai
 7 <120> TITLE OF INVENTION: MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND
CELL
 8        SURVIVAL PATHWAYS
10 <130> FILE REFERENCE: WALLACH=24
12 <140> CURRENT APPLICATION NUMBER: 09/445,223A
13 <141> CURRENT FILING DATE: 1999-12-06
15 <150> PRIOR APPLICATION NUMBER: IL 121011
16 <151> PRIOR FILING DATE: 1997-06-05
18 <150> PRIOR APPLICATION NUMBER: IL 121199
19 <151> PRIOR FILING DATE: 1997-06-30
21 <150> PRIOR APPLICATION NUMBER: IL 121746
22 <151> PRIOR FILING DATE: 1997-09-11
24 <160> NUMBER OF SEQ ID NOS: 3
26 <170> SOFTWARE: PatentIn version 3.3
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 540
30 <212> TYPE: PRT
31 <213> ORGANISM: Homo sapiens
33 <400> SEQUENCE: 1
35 Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr Ile Pro Tyr His
36 1               5                   10                  15
39 Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala Ser Gly Thr Val
40              20                  25                  30
43 Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val Ala Val Lys His
44          35                  40                  45
47 Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg Lys Asp Val Leu
48      50                  55                  60
51 Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser Tyr Ile Phe Pro
52 65                  70                  75                  80
55 Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly Ile Val Thr Glu
56                  85                  90                  95
59 Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His Arg Lys Thr Glu
60              100                 105                 110
63 Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile Leu His Glu Ile
64          115                 120                 125
67 Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro Pro Leu Leu His
68      130                 135                 140
71 His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn Glu Phe His Val
72 145                 150                 155                 160
75 Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met Met Ser Leu Ser
76              165                 170                 175
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 79 Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly Thr Ile Ile Tyr
 80             180               185               190
 83 Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser Arg Ala Ser Ile
 84         195               200               205
 87 Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp Glu Val Leu Ser
 88     210               215               220
 91 Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu Gln Ile Met Tyr
 92 225               230               235               240
 95 Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu Glu Ser Leu Pro
 96             245               250               255
 99 Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu Ile Glu Ser Gly
100             260               265               270
103 Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu Lys Cys Leu Ile
104         275               280               285
107 Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile Thr Phe Leu Glu
108     290               295               300
111 Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser Val Ser Ser Ala
112 305               310               315               320
115 Ile His Leu Cys Asp Lys Lys Lys Met Glu Leu Ser Leu Asn Ile Pro
116             325               330               335
119 Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser Ser Gln Leu His
120             340               345               350
123 Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu Pro Ala Pro Gln
124         355               360               365
127 Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys Tyr Phe Met Lys
128     370               375               380
131 Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser Thr Ile Ser Gly
132 385               390               395               400
135 Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr Pro Cys Ser Ser
136             405               410               415
139 Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser Glu Arg Leu Gln
140         420               425               430
143 Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val
144         435               440               445
147 Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu
148     450               455               460
151 Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys
152 465               470               475               480
155 Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile
156             485               490               495
159 Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn
160         500               505               510
163 Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu Val Val Ser Arg
164         515               520               525
167 Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met
168     530               535               540
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 2098
173 <212> TYPE: DNA
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174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 2
177 ggccattatg gatggatggg cggcgctacg gcgttggcac cagtctctag aaaagaagtc     60
179 agctctggtt cggagaagca gcggctggcg tgggccatcc ggggaatggg cgccctcgtg    120
181 acctagtgtt gcggggcaaa aagggtcttg ccggcctcgc tcgtgcaggg gcgtatctgg    180
183 gcgcctgagc gcggcgtggg agccttggga gccgccgcag caggggggcac acccggaacc   240
185 ggcctgagcg cccgggacca tgaacgggga ggccatctgc agcgccctgc ccaccattcc    300
187 ctaccacaaa ctcgccgacc tgcgctacct gagccgcggc gcctctggca ctgtgtcgtc    360
189 cgcccgccac gcagactggc gcgtccaggt ggccgtgaag cacctgcaca tccacactcc    420
191 gctgctcgac agtgaaagaa aggatgtttt aagagaagct gaaattttac acaaagctag    480
193 atttagttac attttttccaa ttttgggaat ttgcaatgag cctgaatttt tgggaatagt   540
195 tactgaatac atgccaaatg gatcattaaa tgaactccta cataggaaaa ctgaatatcc    600
197 tgatgttgct tggccattga gatttcgcat cctgcatgaa attgcccttg gtgtaaatta    660
199 cctgcacaat atgactcctc ctttacttca tcatgacttg aagactcaga atatcttatt    720
201 ggacaatgaa tttcatgtta agattgcaga tttttggttta tcaaagtggc gcatgatgtc   780
203 cctctcacag tcacgaagta gcaaatctgc accagaagga gggacaatta tttatatgcc    840
205 acctgaaaac tatgaacctg gacaaaaatc aagggccagt atcaagcacg atatatatag     900
207 ctatgcagtt atcacatggg aagtgttatc cagaaaacag ccttttgaag atgtcaccaa    960
209 tcctttgcag ataatgtata gtgtgtcaca aggacatcga cctgttatta atgaagaaag   1020
211 tttgccatat gatatacctc accgagcacg tatgatctct ctaatagaaa gtggatgggc   1080
213 acaaaatcca gatgaaagac catctttctt aaaatgttta atagaacttg aaccagtttt   1140
215 gagaacattt gaagagataa cttttcttga agctgttatt cagctaaaga aaacaaagtt    1200
217 acagagtgtt tcaagtgcca ttcacctatg tgacaagaag aaaatggaat tatctctgaa    1260
219 catacctgta aatcatggtc cacaagagga atcatgtgga tcctctcagc tccatgaaaa   1320
221 tagtggttct cctgaaactt caaggtccct gccagctcct caagacaatg atttttttatc   1380
223 tagaaaagct caagactgtt attttatgaa gctgcatcac tgtcctggaa atcacagttg    1440
225 ggatagcacc atttctggat ctcaaagggc tgcattctgt gatcacaaga ccactccatg   1500
227 ctcttcagca ataataaatc cactctcaac tgcaggaaac tcagaacgtc tgcagcctgg    1560
229 tatagcccag cagtggatcc agagcaaaag ggaagacatt gtgaaccaaa tgacagaagc   1620
231 ctgccttaac cagtcgctag atgcccttct gtccagggac ttgatcatga aagaggacta    1680
233 tgaacttgtt agtaccaagc ctacaaggac ctcaaaagtc agacaattac tagacactac   1740
235 tgacatccaa ggagaagaat ttgccaaagt tatagtacaa aaattgaaag ataacaaaca   1800
237 aatgggtctt cagccttacc cggaaatact tgtggtttct agatcaccat ctttaaattt   1860
239 acttcaaaat aaaagcatgt aagtgactgt ttttcaagaa gaaatgtgtt tcataaaagg   1920
241 atatttatat ctctgttgct ttgactttt ttatataaaa tccgtgagta ttaaagcttw    1980
243 awwraargkt ctttsrktaa atattagtct ccctccatga cactgcagta tttttttaa    2040
245 ttaatacaag taaaaagttg aatttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa       2098
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 4
250 <212> TYPE: PRT
251 <213> ORGANISM: Artificial
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Synthetic
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (1)..(1)
260 <223> OTHER INFORMATION: Residue at postion 1 is modified by an acetyl group.
262 <220> FEATURE:
263 <221> NAME/KEY: misc_feature
```

Input Set : **A:\sequence listing.txt**
Output Set: **N:\CRF4\05062005\I445223A.raw**

264 <222> LOCATION: (4)..(4)
265 <223> OTHER INFORMATION: Residue at postion 4 is modified by
266   a-(4-methyl-coumaryl-7-amide).
268 <220> FEATURE:
269 <221> NAME/KEY: misc_feature
270 <222> LOCATION: (4)..(4)
271 <223> OTHER INFORMATION: Residue at postion 4 is modified by an AC-DEVD-AMC group.
273 <400> SEQUENCE: 3
275 Asp Glu Val Asp
276 1

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/06/2005
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3

VERIFICATION SUMMARY   DATE: 05/06/2005
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